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RAW SEQUENCE LISTING   DATE: 05/02/2002
PATENT APPLICATION: US/10/037,616   TIME: 15:52:56

Input Set : **A:\English Sequence Listing.txt**
Output Set: **N:\CRF3\05022002\J037616.raw**

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  4 <110> APPLICANT: English, Denis
  5        Kovacs, Richard J.
  6        Rizzo, Maria T.
  7        Sliva, Daniel T.
 10 <120> TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic
Use
 13 <130> FILE REFERENCE: 7042-119
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/037,616
C--> 18 <141> CURRENT FILING DATE: 2002-04-19
 21 <150> PRIOR APPLICATION NUMBER: US 60/243,887
 23 <151> PRIOR FILING DATE: 2000-10-27
 26 <160> NUMBER OF SEQ ID NOS: 27
 29 <170> SOFTWARE: PatentIn version 3.1
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 2776
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Homo sapiens
 38 <220> FEATURE:
 39 <221> NAME/KEY: CDS
 40 <222> LOCATION: (244)..(1386)
 41 <223> OTHER INFORMATION:
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 50 cacaaaaagc ctggatcact catcgaacca cccctgaagc cagtgaaggc tctctcgcct     180
 52 cgccctctag cgttcgtctg gagtagcgcc accccggctt cctggggaca cagggttggc     240
 54 acc atg ggg ccc acc agc gtc ccg ctg gtc aag gcc cac cgc agc tcg      288
 55     Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser Ser
 56     1               5                  10                  15
 58 gtc tct gac tac gtc aac tat gat atc atc gtc cgg cat tac aac tac     336
 59 Val Ser Asp Tyr Val Asn Tyr Asp Ile Ile Val Arg His Tyr Asn Tyr
 60                 20                  25                  30
 62 acg gga aag ctg aat atc agc gcg gac aag gag aac agc att aaa ctg     384
 63 Thr Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu
 64             35                  40                  45
 66 acc tcg gtg gtg ttc att ctc atc tgc tgc ttt atc atc ctg gag aac     432
 67 Thr Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn
 68         50                  55                  60
 70 atc ttt gtc ttg ctg acc att tgg aaa acc aag aaa ttc cac cga ccc     480
 71 Ile Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro
 72     65                  70                  75
 74 atg tac tat ttt att ggc aat ctg gcc ctc tca gac ctg ttg gca gga     528
 75 Met Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly
 76 80                  85                  90                  95
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78 gta gcc tac aca gct aac ctg ctc ttg tct ggg gcc acc acc tac aag      576
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80              100             105             110
82 ctc act ccc gcc cag tgg ttt ctg cgg gaa ggg agt atg ttt gtg gcc      624
83 Leu Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala
84              115             120             125
86 ctg tca gcc tcc gtg ttc agt ctc ctc gcc atc gcc att gag cgc tat      672
87 Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr
88              130             135             140
90 atc aca atg ctg aaa atg aaa ctc cac aac ggg agc aat aac ttc cgc      720
91 Ile Thr Met Leu Lys Met Lys Leu His Asn Gly Ser Asn Asn Phe Arg
92       145             150             155
94 ctc ttc ctg cta atc agc gcc tgc tgg gtc atc tcc ctc atc ctg ggt      768
95 Leu Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile Leu Gly
96 160             165             170             175
98 ggc ctg cct atc atg ggc tgg aac tgc atc agt gcg ctg tcc agc tgc      816
99 Gly Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser Ser Cys
100             180             185             190
102 tcc acc gtg ctg ccg ctc tac cac aag cac tat atc ctc ttc tgc acc     864
103 Ser Thr Val Leu Pro Leu Tyr His Lys His Tyr Ile Leu Phe Cys Thr
104             195             200             205
106 acg gtc ttc act ctg ctt ctg ctc tcc atc gtc att ctg tac tgc aga     912
107 Thr Val Phe Thr Leu Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg
108       210             215             220
110 atc tac tcc ttg gtc agg act cgg agc cgc cgc ctg acg ttc cgc aag     960
111 Ile Tyr Ser Leu Val Arg Thr Arg Ser Arg Arg Leu Thr Phe Arg Lys
112       225             230             235
114 aac att tcc aag gcc agc cgc agc tct gag aag tcg ctg gcg ctg ctc    1008
115 Asn Ile Ser Lys Ala Ser Arg Ser Ser Glu Lys Ser Leu Ala Leu Leu
116 240             245             250             255
118 aag acc gta att atc gtc ctg agc gtc ttc atc gcc tgc tgg gca ccg    1056
119 Lys Thr Val Ile Ile Val Leu Ser Val Phe Ile Ala Cys Trp Ala Pro
120             260             265             270
122 ctc ttc atc ctg ctc ctg ctg gat gtg ggc tgc aag gtg aag acc tgt    1104
123 Leu Phe Ile Leu Leu Leu Leu Asp Val Gly Cys Lys Val Lys Thr Cys
124             275             280             285
126 gac atc ctc ttc aga gcg gag tac ttc ctg gtg tta gct gtg ctc aac    1152
127 Asp Ile Leu Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala Val Leu Asn
128       290             295             300
130 tcc ggc acc aac ccc atc att tac act ctg acc aac aag gag atg cgt    1200
131 Ser Gly Thr Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg
132       305             310             315
134 cgg gcc ttc atc cgg atc atg tcc tgc tgc aag tgc ccg agc gga gac    1248
135 Arg Ala Phe Ile Arg Ile Met Ser Cys Cys Lys Cys Pro Ser Gly Asp
136 320             325             330             335
138 tct gct ggc aaa ttc aag cga ccc atc atc gcc ggc atg gaa ttc agc    1296
139 Ser Ala Gly Lys Phe Lys Arg Pro Ile Ile Ala Gly Met Glu Phe Ser
140             340             345             350
142 cgc agc aaa tcg gac aat tcc tcc cac ccc cag aaa gac gaa ggg gac    1344
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PATENT APPLICATION: US/10/037,616   TIME: 15:52:56

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143 Arg Ser Lys Ser Asp Asn Ser Ser His Pro Gln Lys Asp Glu Gly Asp
144         355             360             365
146 aac cca gag acc att atg tct tct gga aac gtc aac tct tct           1386
147 Asn Pro Glu Thr Ile Met Ser Ser Gly Asn Val Asn Ser Ser
148         370             375             380
150 tcctagaact ggaagctgtc cacccaccgg aagcgctctt tacttggtcg ctggccaccc   1446
152 cagtgtttgg aaaaaaatct ctgggcttcg actgctgcca gggaggagct gctgcaagcc   1506
154 agagggagga aggggggagaa tacgaacagc ctggtggtgt cgggtgttgg tgggtagagt   1566
156 tagttcctgt gaacaatgca ctgggaaggg tggagatcag gtcccggcct ggaatatatt   1626
158 ttctaccccc ctggagcttt gattttgcac tgagccaaag gtctagcatt gtcaagctcc   1686
160 taaagggttc atttggcccc tcctcaaaga ctaatgtccc catgtgaaag cgtctctttg   1746
162 tctggagctt tgaggagatg ttttccttca ctttagtttc aaacccaagt gagtgtgtgc   1806
164 acttctgctt ctttagggat gccctgtaca tcccacaccc caccctccct tcccttcata   1866
166 cccctcctca acgttctttt actttatact ttaactacct gagagttatc agagctgggg   1926
168 ttgtggaatg atcgatcatc tatagcaaat aggctatgtt gagtacgtag gctgtgggaa   1986
170 gatgaagatg gtttggaggt gtaaaacaat gtccttcgct gaggccaaag tttccatgta   2046
172 agcgggatcc gtttttggga atttggttga agtcactttg atttctttaa aaaacatctt   2106
174 ttcaatgaaa tgtgttacca tttcatatcc attgaagccg aaatctgcat aaggaagccc   2166
176 actttatcta aatgatatta gccaggatcc ttggtgtcct aggagaaaca gacaagcaaa   2226
178 acaaagtgaa aaccgaatgg attaactttt gcaaaccaag ggagatttct tagcaaatga   2286
180 gtctaacaaa tatgacatct gtctttggca cttttgttga tgtttatttc agaatgttgt   2346
182 gtgattcatt tcaagcaaca acatggttgt attttgttgt gttaaaagta cttttcttga   2406
184 tttttgaatg tatttgtttc agcagaagtc attttattgg atttttctaa cccgtgttaa   2466
186 caccattgaa tgtgtatttc ttaagaaaat accaccctct tgtgcccctta aaagcattac   2526
188 tttaactggt agggaacgcc agaaactttt cagtccagct attcattaga tagtaattga   2586
190 agatatgtat aaatattaca aagaataaaa atatattact gtctctttag tatggttttc   2646
192 agtgcaatta aaccgagaga tgtcttgttt ttttaaaaag aatagtattt aataggtttc   2706
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217 cgttcttgcg agccggcctg caggaggcga ggctcccctg gcctcccgca cccagcggcg    180
219 gaccgagccc ctggagggaa gttgccgcag ccgcccgggc cgccggccct cctgtcccgc    240
221 gccaggtaca cagcttctcc tagcatgact tcgatctgat cagcaaacaa gaaaatttgt    300
223 ctcccgtagt tctggggcgt gttcaccacc tacaaccaca gagctgtc atg gct gcc     357
224                                                        Met Ala Ala
225                                                        1
227 atc tct act tcc atc cct gta att tca cag ccc cag ttc aca gcc atg     405
228 Ile Ser Thr Ser Ile Pro Val Ile Ser Gln Pro Gln Phe Thr Ala Met
229     5               10              15
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232 Asn Glu Pro Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe Phe Tyr Asn
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235 cga agt gga aag cat ctt gcc aca gaa tgg aac aca gtc agc aag ctg      501
236 Arg Ser Gly Lys His Leu Ala Thr Glu Trp Asn Thr Val Ser Lys Leu
237             40                  45                  50
239 gtg atg gga ctt gga atc act gtt tgt atc ttc atc atg ttg gcc aac      549
240 Val Met Gly Leu Gly Ile Thr Val Cys Ile Phe Ile Met Leu Ala Asn
241         55                  60                  65
243 cta ttg gtc atg gtg gca atc tat gtc aac cgc cgc ttc cat ttt cct      597
244 Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe His Phe Pro
245         70                  75                  80
247 att tat tac cta atg gct aat ctg gct gct gca gac ttc ttt gct ggg      645
248 Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly
249         85                  90                  95
251 ttg gcc tac ttc tat ctc atg ttc aac aca gga ccc aat act cgg aga      693
252 Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn Thr Arg Arg
253 100             105                 110                 115
255 ctg act gtt agc aca tgg ctc ctt cgt cag ggc ctc att gac acc agc      741
256 Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile Asp Thr Ser
257             120                 125                 130
259 ctg acg gca tct gtg gcc aac tta ctg gct att gca atc gag agg cac      789
260 Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile Glu Arg His
261             135                 140                 145
263 att acg gtt ttc cgc atg cag ctc cac aca cgg atg agc aac cgg cgg      837
264 Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser Asn Arg Arg
265         150                 155                 160
267 gta gtg gtg gtc att gtg gtc atc tgg act atg gcc atc gtt atg ggt      885
268 Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile Val Met Gly
269     165                 170                 175
271 gct ata ccc agt gtg ggc tgg aac tgt atc tgt gat att gaa aat tgt      933
272 Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile Glu Asn Cys
273 180                 185                 190                 195
275 tcc aac atg gca ccc ctc tac agt gac tct tac tta gtc ttc tgg gcc      981
276 Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val Phe Trp Ala
277             200                 205                 210
279 att ttc aac ttg gtg acc ttt gtg gta atg gtg gtt ctc tat gct cac     1029
280 Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu Tyr Ala His
281             215                 220                 225
283 atc ttt ggc tat gtt cgc cag agg act atg aga atg tct cgg cat agt     1077
284 Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser Arg His Ser
285         230                 235                 240
287 tct gga ccc cgg cgg aat cgg gat acc atg atg agt ctt ctg aag act     1125
288 Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu Leu Lys Thr
289     245                 250                 255
291 gtg gtc att gtg ctt ggg gcc ttt atc atc tgc tgg act cct gga ttg     1173
292 Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr Pro Gly Leu
293 260                 265                 270                 275
295 gtt ttg tta ctt cta gac gtg tgc tgt cca cag tgc gac gtg ctg gcc     1221
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300 Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser Ala Met Asn
301          295             300             305
303 ccc atc att tac tcc tac cgc gac aaa gaa atg agc gcc acc ttt agg      1317
304 Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala Thr Phe Arg
305          310             315             320
307 cag atc ctc tgc tgc cag cgc agt gag aac ccc acc ggc ccc aca gaa      1365
308 Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly Pro Thr Glu
309          325             330             335
311 ggc tca gac cgc tcg gct tcc tcc ctc aac cac acc atc ttg gct gga      1413
312 Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile Leu Ala Gly
313 340             345             350             355
315 gtt cac agc aat gac cac tct gtg gtt tagaacggaa actgagatga            1460
316 Val His Ser Asn Asp His Ser Val Val
317              360
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321 ggtggggtgt gagagaggag aaaagtcaac tcatgtactt aaacactaac caatgacagt    1580
323 atttgttcct ggaccccaca agacttgata tatattgaaa attagcttat gtgacaaccc    1640
325 tcatcttgat ccccatccct tctgaaagta ggaagttgga gctcttgcaa tggaattcaa    1700
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335 cccttacata ggaaaactgt aagttggaat tatcttttgt ttagaaagca tgcatgtaat    2000
337 gtatgtatgc agtatgcctt acttaaaaag attaaaagga tactaatgtt aaatcttcta    2060
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341 taatcacaat attaactgtt taattaaaat gttgtaacaa gtataaaaca gggaatgtaa    2180
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351 gcaacccca tgtatgccta tatgtgtatt gtatacttt tttacataat tggagtcata     2480
353 ctgtaaacag ttttataagt agatctttt cattgcaaaa ttgccacatt ttcttatggc    2540
355 attaaaaatt ttacaaaaac ataattttaa tggctatatt atattccatt taatggatgc    2600
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371 <223> OTHER INFORMATION:
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VERIFICATION SUMMARY   DATE: 05/02/2002
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L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date